IN THE SPECIFICATION:

Please insert the attached substitute sequence listing after the specification but before the claims.

On pages 18 and 19 of the specification, please replace Tables 1 and 2 with the following new tables:

Table 1. Estimation of the VEGF protein family MHCI associated peptides in the context of HLAA.0201

A.- Using BIMAS software														
VEGF-A			VEGF-B			VEGF-C			VEGF-D			PIGF		
SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd
27	LLSWVHWSL	**272**	**37**	LLLAALLQL	**309**	**47**	YLSKTLFEI	**640**	**57**	FMMLYVQLV	**1966**	**67**	RLFPCFLQL	**150**
28	ALLLYLHHA	**42**	**38**	QLAPAQAPV	**70**	**48**	TLFEITVPL	**324**	**58**	KLWRCRLRL	**620**	**68**	VVSEYPSEV	**42**
29	WSLALLLYL	**30**	**39**	QLVPSCVTV	**70**	**49**	VLYPEYWKM	**304**	**59**	QLFEISVPL	**324**	**69**	VMRLFPCFL	**42**
30	FLQHNKCEC	**23**	**40**	LMGTVAKQL	**26**	**50**	CMNTSTSYL	85	**60**	YISKQLFEI	**88**	**70**	RALERLVDV	**34**
31	WVHWSLALL	20	**41**	LLAALLQLA	**19**	**51**	KLFPSQCGA	**64**	**61**	CMNTSTSYI	41	**71**	VELTFSQHV	**32**
32	FLLSWVHWS	**16**	**42**	LLQLAPAQA	**8**	**52**	LLGFFSVAC	32	**62**	VLQEENPLA	35	**72**	AVPPQQWAL	**14**
33	RQLELNERT	**6**	**43**	VVSWIDVYT	6	**53**	SLPATLPQC	**11**	**63**	WVVVNVFMM	27	**73**	LQLLAGLAL	**14**
34	NITMQIMRI	**3**	**44**	CVPTGQHQV	**6**	**54**	GLQCMNTST	**7**	**64**	VNVFMMLYV	10	**74**	RSGDRPSYV	**10**
35	YCHPIETLV	**2**	**45**	KQLVPSCVT	4	**55**	AAFESGLDL	**4**	**65**	SLICMNTST	**7**	**75**	LLAGLALPA	8
36	IEYIFKPSC	2	**46**	VVVPLTVEL	**3**	**56**	EQLRSVSSV	4	**66**	CVLQEENPL	7	**76**	CVPVETANV	**6**
B.- Using SYFPEITHI software														
VEGF-A			VEGF-B			VEGF-C			VEGF-D			PIGF		
SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score
77	LLSWVHWSL	**24**	**87**	LLLAALLQL	**29**	**97**	TLFEITVPL	**27**	**107**	FMMLYVQLV	**25**	**117**	ALERLVDVV	**26**
78	ALLLYLHHA	**24**	**88**	QLAPAQAPV	**26**	**98**	DLEEQLRSV	**26**	**108**	QLFEISVPL	**25**	**118**	RLFPCFLQL	**24**
79	WVHWSLALL	**20**	**89**	QLVPSCVTV	**26**	**99**	YLSKTLFEI	**26**	**109**	YISKQLFEI	**24**	**119**	RALERLVDV	**24**
80	SLALLLYLH	**20**	**90**	VVVPLTVEL	**24**	**100**	ALLPGPREA	24	**110**	KLWRCRLRL	**23**	**120**	LLAGLALPA	**22**
81	SYCHPIETL	19	**91**	LLRRLLLAA	**23**	**101**	CMNTSTSYL	**21**	**111**	RAASSLEEL	22	**121**	LAGLALPAV	**22**
82	NITMQIMRI	**19**	**92**	LLAALLQLA	**23**	**102**	DICGPNKEL	21	**112**	SLEELLRIT	22	**122**	VMRLFPCFL	**20**
83	FLLSWVHWS	**18**	**93**	FLRCQGRGL	22	**103**	AAAAFESGL	**20**	**113**	ATFYDIETL	22	**123**	CFLQLLAGL	**20**
84	WSLALLLYL	**18**	**94**	LTVELMGTV	**21**	**104**	AAFESGLDL	**20**	**114**	EISVPLTSV	22	**124**	QLLAGLALP	**20**
85	HPIETLVDI	**18**	**95**	LRRLLLAAL	20	**105**	VLYPEYWKM	**20**	**115**	SLICMNTST	**20**	**125**	SAGNGSSEV	20
86	CNDEGLECV	18	**96**	LMGTVAKQL	**19**	**106**	IIRRSLPAT	20	**116**	VPLTSVPEL	20	**126**	VVSEYPSEV	**20**

Note: Values in bold correspond to those peptides or their regions, which coincide in both predictions.

Table 2. Estimation of VEGF family receptors MHCI associated peptides in the context of HLAA.0201

A.- Using BIMAS software														
VEGFR-1			VEGFR-2			VEGFR-3			NRP-1			NRP-2		
SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd	SEQ ID	Secuencia	Kd
127	FLYRDVTWI	**1942**	**137**	VLLWEIFSL	**1792**	**147**	VLLWEIFSL	**1793**	**157**	GLLRFVTAV	**2249**	**167**	WMYDHAKWL	**5121**
128	VLLWEIFSL	**1792**	**138**	SLQDQGDYV	**769**	**148**	RLLEEKSGV	**1055**	**158**	VLLGAVCGV	**1006**	**168**	ILQFLIFDL	**484**
129	KLLRGHTLV	**901**	**139**	VLLAVALWL	**739**	**149**	VLWPDGQEV	**981**	**159**	WMPENIRLV	**436**	**169**	YLQVDLRFL	**247**
130	GLLTCEATV	**257**	**140**	AMFFWLLLV	**427**	**150**	NLTDLLVNV	656	**160**	GILSMVFYT	**278**	**170**	ALYFSRHQV	**223**
131	TLFWLLLTL	182	**141**	VIAMFFWLL	**270**	**151**	KQAERGKWV	**557**	**161**	LLCAVLALV	272	**171**	NMLGMLSGL	**131**
132	ILLSENNVV	**179**	**142**	ILLSEKNVV	**179**	**152**	GVIAVFFWV	369	**162**	VLLHKSLKL	134	**172**	WLYTLDPIL	**129**
133	TLNLTIMNV	**160**	**143**	LLAVALWLC	146	**153**	KLVIQNANV	**243**	**163**	GMLGMVSGL	131	**173**	DIWDGIPHV	**56**
134	CVAATLFWL	**137**	**144**	KNLDTLWKL	**128**	**154**	ALWNSAAGL	**177**	**164**	FQLTGGTTV	120	**174**	KMEIILQFL	**44**
135	LLSIKQSNV	**118**	**145**	AVIAMFFWL	113	**155**	TLSLSIPRV	**160**	**165**	VLATEKPTV	**118**	**175**	VLNKLHAPL	36
136	SLQDSGTYA	112	**146**	LLLVIILRT	**108**	**156**	SQHDLGSYV	159	**166**	GPFLFIKFV	81	**176**	LLGATCAGL	**36**
B.- Using SYFPEITHI software														
VEGFR-1			VEGFR-2			VEGFR-3			NRP-1			NRP-2		
SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score	SEQ ID	Secuencia	Score
177	TLFWLLLTL	**29**	**187**	VLLWEIFSL	**29**	**197**	VLLWEIFSL	**29**	**207**	VLLGAVCGV	**30**	**217**	NMLGMLSGL	**27**
178	VLLWEIFSL	**29**	**188**	LLVIILRTV	**28**	**198**	SIPGLNVTL	**27**	**208**	GLLRFVTAV	**29**	**218**	ILQFLIFDL	**26**
179	ILGPGSSTL	**28**	**189**	GLFCKTLTI	**26**	**199**	NLTDLLVNV	**27**	**209**	LLCAVLALV	**28**	**219**	DIWDGIPHV	**26**
180	LLCALLSCL	**27**	**190**	SIMYIVVVV	**26**	**200**	VLWPDGQEV	26	**210**	GMLGMVSGL	**28**	**220**	YLQVDLRFL	**26**
181	GLLTCEATV	27	**191**	IILVGTAVI	**26**	**201**	LLPRKSLEL	**26**	**211**	ALGVLLGAV	28	**221**	TLDPILITI	**26**
182	LLRGHTLVL	**27**	**192**	ALMSELKIL	**26**	**202**	ALWNSAAGL	26	**212**	VLLHKSLKL	27	**222**	ILAKPKMEI	**25**
183	ALMTELKIL	**26**	**193**	AASVGLPSV	25	**203**	IMDPGEVPL	**26**	**213**	VLATEKPTV	26	**223**	VLNKLHAPL	**25**
184	KLLRGHTLV	**25**	**194**	SISNLNVSL	**25**	**204**	RLWLCLGLL	**25**	**214**	QLTGGTTVL	25	**224**	LLGATCAGL	**25**
185	TLNLTIMNV	**25**	**195**	AMFFWLLLV	25	**205**	LIYFYVTTI	**25**	**215**	VLLGAVCGV	**30**	**225**	ALYFSRHQV	23
186	ILLSENNVV	25	**196**	ILLSEKNVV	**25**	**206**	LLEGQPVLL	25	**216**	GLLRFVTAV	29	**226**	GIGMRLEVL	**23**

Note: Values in bold correspond to those peptides or their regions, which coincide in both predictions.

On page 21 of the specification, please replace the paragraph beginning on line 9 with the following:

In the case of the extracellular domains 1 to 3 SEQ ID NO. ~~27~~ 23 and SEQ ID NO: ~~28~~ 24 ~~(for domains 1-3) and SEQ ID NO: 29 and SEQ ID NO: 30 (for domain 3 alone)~~, the primers used correspond to sequences SEQ ID NO: 9 and SEQ ID NO: 10. After digestion of the amplified fragment (943bp) ~~SEQ ID NO: 25 and SEQ ID NO: 26~~ with endonucleases BamHI and EcoRI, the cDNA coding 1-3 domains of KDR was purified, and cloned in pAECΔ2 vector. Clones positive by restriction analysis were verified by sequencing of the corresponding DNA. The cDNA corresponding to KDR 1-3 was then subcloned KpnI/EcoRV in the already described pMAE5Δ5 vector (pMAE5Δ5 KDR1-3).

For the cloning of transmembrane and cytostolic regions of the receptor (SEQ ID NO: 25 and SEQ ID NO: 26) a two-step strategy was designed. For the insertion of the first segment, the primers corresponding to SEQ ID NO: 11 and SEQ ID NO: 12 were used. After the XbaI/BgIII digestion of this 747bp segment, the product was cloned in the pMAE5 vector, previously digested with the same enzymes, obtaining the plasmid PMAE5 KDR 747. This plasmid was digested BgIII/NotI in order to insert the remaining carboxi-terminal fragment of 1091bp that was amplified using the primers corresponding to sequences SEQ ID NO: 13 and SEQ ID NO: 14. Clones positive by restriction analysis were verified by DNA sequencing and denominated pMAE5 KDR C.